

Appl. No. : 09/817,014
Filed : March 23, 2001

AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method for identifying and/or quantifying an organism or part of an organism in a sample by detecting a nucleotide sequence ~~characteristic~~ specific of said organism, wherein said specific nucleotide sequence ~~is homologous to~~ presents a homology higher than 60% with at least 4 other homologous nucleotide sequences from other organisms comprising:

amplifying or copying said specific nucleotide sequence into target nucleotide sequence using primer pairs which are capable of amplifying at least two of said homologous nucleotide sequences from other organisms;

contacting said ~~amplified or copied~~ target nucleotide sequence with single-stranded capture nucleotide sequences, said single-stranded capture nucleotide sequences being covalently bound in an array to an insoluble solid support via a spacer which is at least 6.8 nm in length, wherein said array comprises at least 4 different bound single-stranded capture nucleotide sequences/cm² of solid support surface and wherein said capture nucleotide sequences comprise a nucleotide sequence of about ~~10~~ 15 to about ~~60~~ 40 bases which is able to specifically bind to said target nucleotide sequence without binding to said at least 4 homologous nucleotide sequences; and

detecting specific hybridization of said target nucleotide sequence to said capture nucleotide sequences.

2. **(Previously presented)** The method according to claim 1, wherein the amplified nucleotide sequence is a DNA nucleotide sequence.

3. **(Canceled)**

4. **(Previously presented)** The method according to claim 1, wherein the amplified nucleotide sequences are mRNA first reverse transcribed into cDNA and then amplified using said primer pair which is capable of amplifying at least two of said homologous mRNA in said sample.

5-7. **(Canceled)**

8. **(Canceled)**

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9. **(Previously presented)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 10 fmoles per cm² of solid support surface.

10. **(Previously presented)** The method according to claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 30%.

11. **(Canceled)**

12. **(Previously presented)** The method according to claim 1, wherein other primers are present in the amplification step for the amplification of another nucleotide sequence.

13. **(Previously presented)** The method according to claim 1, wherein the insoluble solid support is selected from the group consisting of: glasses, electronic devices, silicon supports, plastic supports, compact discs, filters, filters, gel layers, and metallic supports.

14. **(Previously presented)** The method according to claim 1, wherein the nucleotide sequence to be identified and/or quantified is an RNA sequence submitted to a reverse transcription of its 3' or 5' end by using a consensus primer.

15. **(Previously presented)** The method according to claim 1, wherein the nucleotide sequence to be identified and/or quantified are from the *FemA* gene of Staphylococci species selected from the group consisting of: *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* and *S. haemolyticus*.

16. **(Previously presented)** The method according to claim 1, wherein the solid support also bears capture nucleotide sequences specific of the homologous sequences specific for the binding with the homologous target nucleotide sequence together with a consensus sequence able to bind to said target nucleotide sequence and to said at least 4 homologous nucleotide sequences.

17. **(Original)** The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a Staphylococcus genus identification.

18. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the *MAGE* gene family.

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19. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the *HLA-A* genes family.

20. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

21. **(Previously presented)** The method according to claim 1, wherein the sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

22. **(Previously presented)** The method according to claim 1, wherein the sequence to be detected and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

23. **(Previously presented)** The method according to claim 1, wherein the sequence to be detected and/or quantified in the sample belongs to the cytochrome p450 forms family.

24-37. **(Withdrawn)**.

38. **(Previously presented)** The method of Claim 1, wherein said nucleotide sequence to be identified and/or quantified originates from a microorganism.

39. **(Canceled)**

40. **(Previously presented)** The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is more than about 100 fmoles per cm² of solid support surface.

41. **(Canceled)**

42. **(Previously presented)** The method according to claim 1, wherein the target nucleotide sequence- presents a homology with other homologous nucleotide sequences higher than 80%.

43. **(Previously presented)** The method according to claim 1, wherein the spacer is a non-specific nucleotide sequence of at least 20 nucleotides.

44. **(Previously presented)** The method of Claim 12, wherein said other nucleotide sequence is an antibiotic resistance determining sequence.

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45. **(Previously presented)** The method of Claim 1, wherein said organism is identified or quantitated by detecting a single spot signal at one specific location on said insoluble solid support.